

Fig. 1(A)

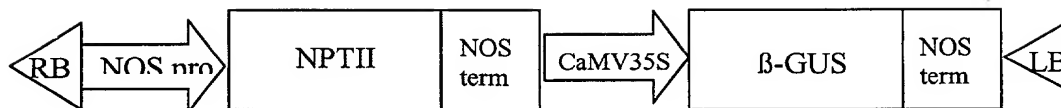


Fig. 1(B)

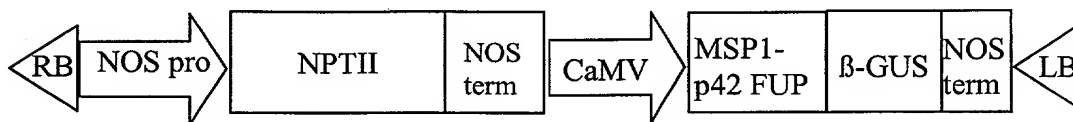


Fig. 1(C)

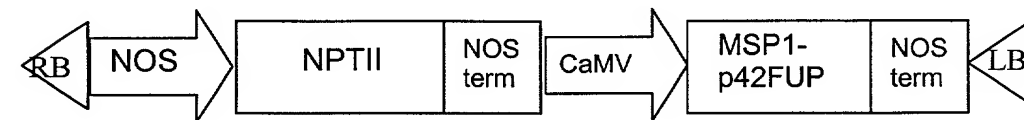
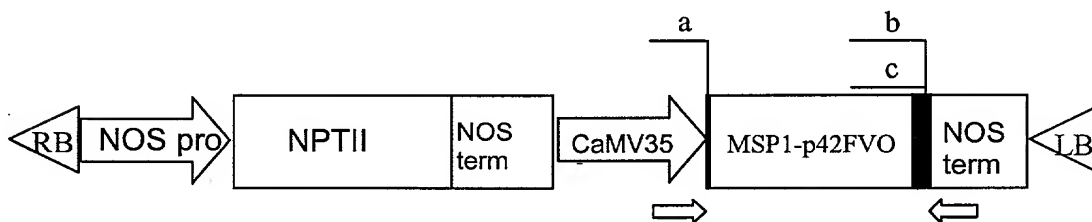


Fig. 1(D)



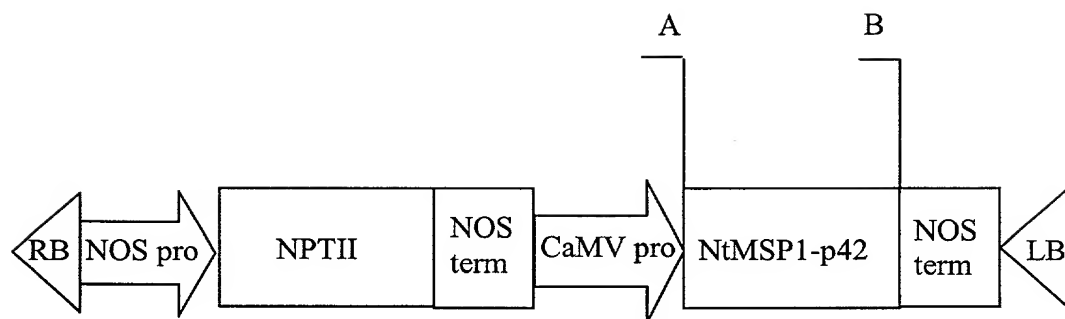


Fig. 2

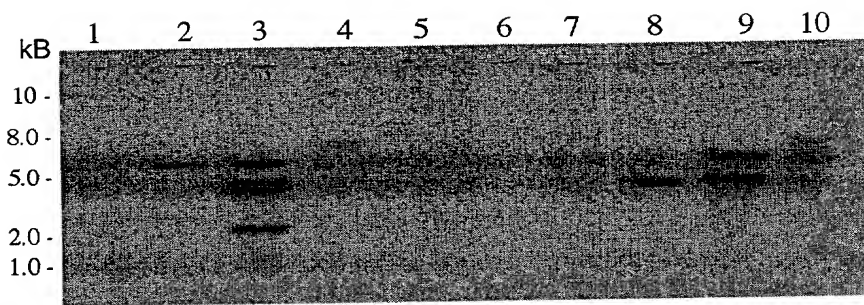


Fig. 3(A)

← MSP1-p42a
← MSP1-p42b

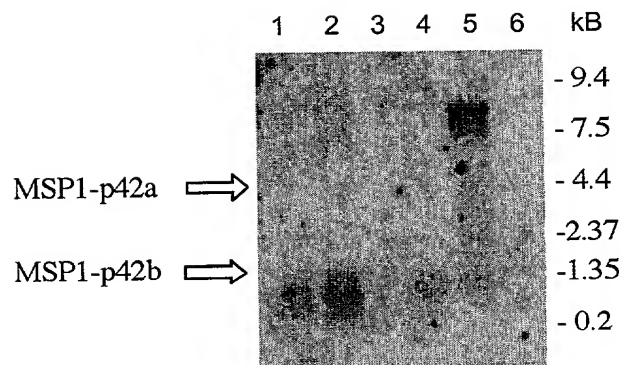


Fig. 3(B)

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Fig. 4(A)

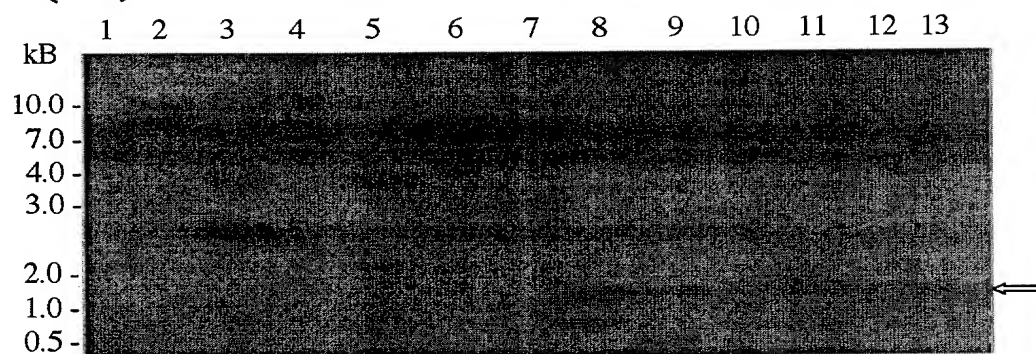


Fig. 4(B)

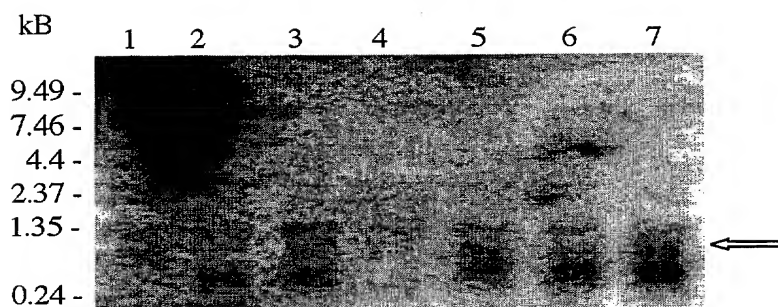


Fig. 5(A)

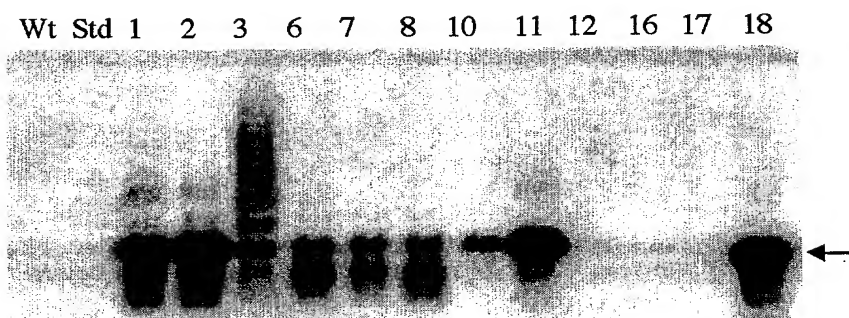
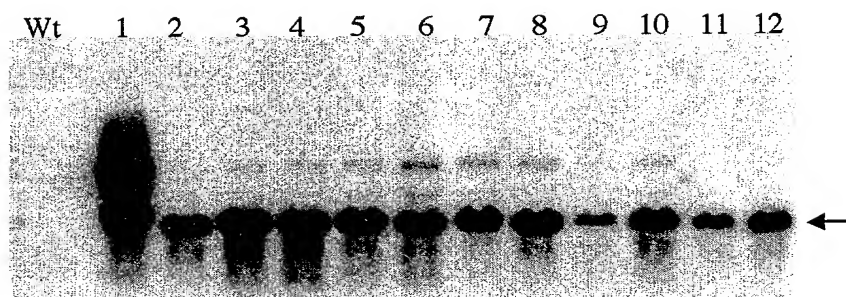


Fig. 5(B)



2014-04-14 14:58:00

Fig. 6(A)

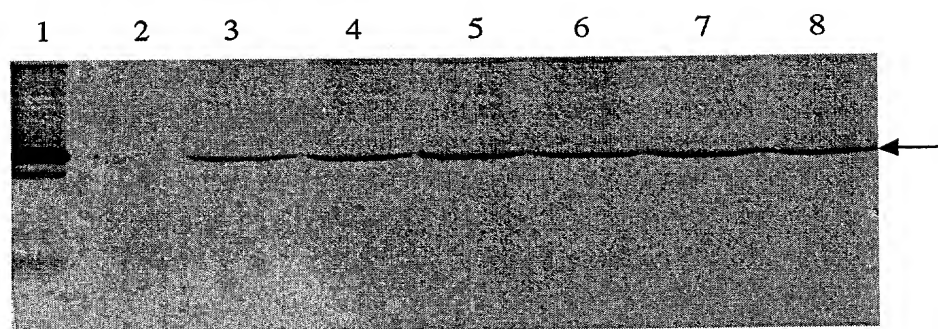
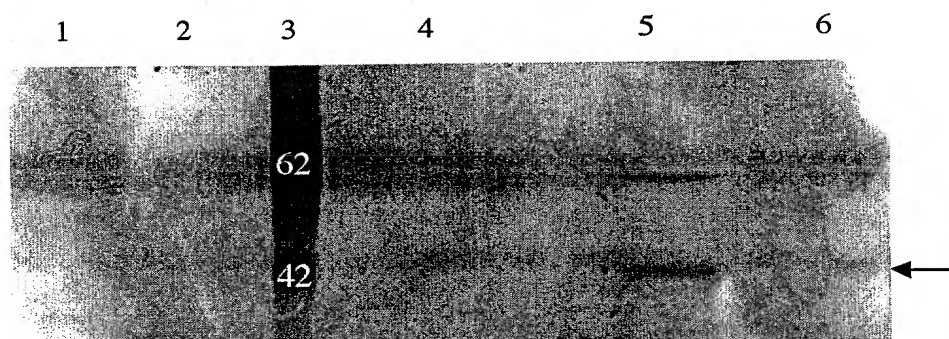


Fig. 6(B)

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Fig. 7(A)

MSP1.p42 FUP

401 AAAATGATATTAAAT TTGCACAGGA AGGTATAAG TTATTATGAAAAGGTT
601 AACATTGAGAC CTTATACAATAAC TTAGTTAATAAAAT TGACGATTACTT
951 TCCAGAAAAT TCTGGATGTTTCAGAC ATTTAGATGAAAG AGAAGAATGTA

MSP1.p42FVO

181 AATTTCAAAATG TTTTAGAATCAGATTTA ATTCCATATAAAG ATTTA
230 ACATCAAGTAATT ATGTTGTCAAAGATCCA TATAAATTTCTTAATAAA
277 GAAAAAAGAGA TAAATTCTTAAGCAGTTA TAATTATATTAAGGATTC

Fig. 7(B)

A	E	F	D	N	I	L	S	D	N	I	L	S	G	F	E	N	E	18
GCC	GAA	TTC	GAC	AAC	ATC	CTC	AGT	GAC	AAC	ATC	CTC	AGT	GGC	TTC	GAG	AAC	GAG	54
Y	D	V	I	Y	L	K	P	L	A	G	V	Y	R	S	L	K	K	36
TAC	GAC	GTA	ATC	TAC	CTA	AAG	CCC	CTT	GCC	GGT	GTC	TAC	CGT	TCA	TTG	AAG	AAA	108
Q	I	E	K	N	I	F	T	F	N	L	N	L	N	D	I	L	N	54
CAG	ATA	GAA	AAG	AAT	ATT	TTC	ACG	TTC	AAC	CTC	AAC	CTA	AAT	GAC	ATC	CTC	AAC	162
S	R	L	K	K	R	K	Y	F	L	D	V	L	E	S	D	L	M	72
TCG	CGC	CTC	AAG	AAG	CGA	AAA	TAC	TTC	CTC	GAC	GTG	TTG	GAA	TCC	GAC	CTT	ATG	216
Q	F	K	H	I	S	S	N	E	Y	I	I	E	D	S	F	K	L	90
CAA	TTC	AAG	CAC	ATT	AGC	TCT	AAC	GAG	TAC	ATC	ATA	GAG	GAC	AGC	TTC	AAG	CTC	270
L	N	S	E	Q	K	N	T	L	L	K	S	Y	K	Y	I	K	E	108
TTG	AAT	TCA	GAA	CAG	AAG	AAC	ACC	CTC	CTA	AAG	TCC	TAC	AAA	TAC	ATT	AAG	GAG	324
S	V	E	N	D	I	K	F	A	Q	E	G	I	S	Y	Y	E	K	126
TCT	GTT	GAG	AAC	GAC	ATC	AAG	TTC	GCC	CAG	GAA	GGA	ATT	AGC	TAC	TAT	GAG	AAA	378
V	L	A	K	Y	K	D	D	L	E	S	I	K	K	V	I	K	E	144
GTC	CTG	GCT	AAA	TAC	AAG	GAC	GAC	TTG	GAA	AGC	ATT	AAG	AAG	GTA	ATC	AAA	GAA	432
E	K	E	K	F	P	S	S	P	P	T	T	P	P	S	P	A	K	162
GAG	AAG	GAA	AAG	TTT	CCG	AGC	TCT	CCA	CCC	ACA	ACT	CCC	CCA	TCG	CCT	GCA	AAG	486
T	D	E	Q	K	K	E	S	K	F	L	P	F	L	T	N	I	E	180
ACC	GAC	GAG	CAG	AAA	AAA	GAA	AGT	AAG	TTC	CTT	CCA	TTC	CTC	ACC	AAC	ATC	GAA	540
T	L	Y	N	N	L	V	N	K	I	D	D	Y	L	I	N	L	K	198
ACT	CTA	TAT	AAC	AAC	CTG	GTG	AAC	AAG	ATT	GAT	GAC	TAC	TTA	ATC	AAC	TTG	AAG	594
A	K	I	N	D	C	N	V	E	K	D	E	A	H	V	K	I	T	216
GCG	AAA	ATT	AAT	GAC	TGT	AAC	GTC	GAA	AAG	GAT	GAA	GCC	CAC	GTT	AAG	ATC	ACC	648
K	L	S	D	L	K	A	I	D	D	K	I	D	L	F	K	N	H	234
AAG	CTT	TCC	GAT	CTC	AAA	GCC	ATC	GAC	GAT	AAG	ATT	GAC	CTG	TTT	AAG	AAC	CAC	702
N	D	F	D	A	I	K	K	L	I	N	D	D	T	K	K	D	M	252
AAC	GAT	TTC	GAC	GCA	ATC	AAA	AAG	TTG	ATC	AAC	GAC	GAT	ACT	AAG	AAA	GAC	ATG	756
L	G	K	L	L	S	T	G	L	V	Q	N	F	P	N	T	I	I	270
CTT	GGA	AAA	CTG	CTG	TCG	ACA	GGC	TTG	GTC	CAA	AAC	TTC	CCG	AAC	ACC	ATT	ATA	810
S	K	L	I	E	G	K	F	Q	D	M	L	N	I	S	Q	H	Q	288
AGC	AAG	CTG	ATC	GAA	GGA	AAG	TTT	CAG	GAT	ATG	CTG	AAC	ATC	TCT	CAG	CAT	CAA	864
C	V	K	K	Q	C	P	E	N	S	G	C	F	R	H	L	D	E	306
TGC	GTG	AAG	AAG	CAA	TGT	CCC	GAG	AAT	TCA	GGT	TGC	TTC	CGC	CAC	TTA	GAC	GAA	918
R	E	E	C	K	C	L	L	N	Y	K	Q	E	G	D	K	C	V	324
AGG	GAG	GAA	TGT	AAA	TGC	CTG	CTG	AAT	TAT	AAA	CAG	GAA	GGA	GAC	AAG	TGC	GTA	972
E	N	P	N	P	T	C	N	E	N	N	G	G	C	D	A	D	A	342
GAG	AAT	CCT	AAC	CCA	ACC	TGT	AAC	GAA	AAT	AAC	GGT	GGC	TGC	GAT	GCT	GAC	GCT	1026
K	C	T	E	E	D	S	G	S	N	G	K	K	I	T	C	E	C	360
AAG	TGT	ACC	GAG	GAG	GAC	AGC	GGT	TCC	AAT	GGC	AAG	AAA	ATA	ACT	TGC	GAA	TGC	1080
T	K	P	D	S	Y	P	L	F	D	G	I	F	C	S	H	D	E	378
ACG	AAG	CCC	GAT	AGT	TAC	CCT	CTC	TTC	GAC	GGT	ATC	TTC	TGC	TCC	CAT	GAT	GAG	1134
L	*	E	L	T														383
CTT	TAA	GAG	CTC	ACC														

Fig. 8

R	I	Q	G	D	I	T	M	D	N	I	L	S	G	F	E	N	E	18
CGG	ATC	CAA	GGA	GAT	ATA	ACA	ATG	GAC	AAC	ATC	CTC	AGT	GGC	TTC	GAG	AAC	GAG	54
Y	D	V	I	Y	L	K	P	L	A	G	V	Y	R	S	L	K	K	36
TAC	GAC	GTA	ATC	TAC	CTA	AAG	CCC	CTT	GCC	GGT	GTC	TAC	CGT	TCA	TTG	AAG	AAA	108
Q	I	E	K	N	I	F	T	F	N	L	N	L	N	D	I	L	N	54
CAG	ATA	GAA	AAG	AAT	ATT	TTC	ACG	TTC	AAC	CTC	AAC	CTA	AAT	GAC	ATC	CTC	AAC	162
S	R	L	K	K	R	K	Y	F	L	D	V	L	E	S	D	L	M	72
TCG	CGC	CTC	AAG	AAG	CGA	AAA	TAC	TTC	CTC	GAC	GTG	TTG	GAA	TCC	GAC	CTT	ATG	216
Q	F	K	H	I	S	S	N	E	Y	I	I	E	D	S	F	K	L	90
CAA	TTC	AAG	CAC	ATT	AGC	TCT	AAC	GAG	TAC	ATC	ATA	GAG	GAC	AGC	TTC	AAG	CTC	270
L	N	S	E	Q	K	N	T	L	L	K	S	Y	K	Y	I	K	E	108
TTG	AAT	TCA	GAA	CAG	AAG	AAC	ACC	CTC	CTA	AAG	TCC	TAC	AAA	TAC	ATT	AAG	GAG	324
S	V	E	N	D	I	K	F	A	Q	E	G	I	S	Y	Y	E	K	126
TCT	GTT	GAG	AAC	GAC	ATC	AAG	TTC	GCC	CAG	GAA	GGA	ATT	AGC	TAC	TAT	GAG	AAA	378
V	L	A	K	Y	K	D	D	L	E	S	I	K	K	V	I	K	E	144
GTC	CTG	GCT	AAA	TAC	AAG	GAC	GAC	TTG	GAA	AGC	ATT	AAG	AAG	GTA	ATC	AAA	GAA	432
E	K	E	K	F	P	S	S	P	P	T	T	P	P	S	P	A	K	162
GAG	AAG	GAA	AAG	TTT	CCG	AGC	TCT	CCA	CCC	ACA	ACT	CCC	CCA	TCG	CCT	GCA	AAG	486
T	D	E	Q	K	K	E	S	K	F	L	P	F	L	T	N	I	E	180
ACC	GAC	GAG	CAG	AAA	AAA	GAA	AGT	AAG	TTC	CTT	CCA	TTC	CTC	ACC	AAC	ATC	GAA	540
T	L	Y	N	N	L	V	N	K	I	D	D	Y	L	I	N	L	K	198
ACT	CTA	TAT	AAC	AAC	CTG	GTG	AAC	AAG	ATT	GAT	GAC	TAC	TTA	ATC	AAC	TTG	AAG	594
A	K	I	N	D	C	N	V	E	K	D	E	A	H	V	K	I	T	216
GCG	AAA	ATT	AAT	GAC	TGT	AAC	GTC	GAA	AAG	GAT	GAA	GCC	CAC	GTT	AAG	ATC	ACC	648
K	L	S	D	L	K	A	I	D	D	K	I	D	L	F	K	N	H	234
AAG	CTT	TCC	GAT	CTC	AAA	GCC	ATC	GAC	GAT	AAG	ATT	GAC	CTG	TTT	AAG	AAC	CAC	702
N	D	F	D	A	I	K	K	L	I	N	D	D	T	K	K	D	M	252
AAC	GAT	TTC	GAC	GCA	ATC	AAA	AAG	TTG	ATC	AAC	GAC	GAT	ACT	AAG	AAA	GAC	ATG	756
L	G	K	L	L	S	T	G	L	V	Q	N	F	P	N	T	I	I	270
CTT	GGA	AAA	CTG	CTG	TCG	ACA	GGC	TTG	GTC	CAA	AAC	TTC	CCG	AAC	ACC	ATT	ATA	810
S	K	L	I	E	G	K	F	Q	D	M	L	N	I	S	Q	H	Q	288
AGC	AAG	CTG	ATC	GAA	GGA	AAG	TTT	CAG	GAT	ATG	CTG	AAC	ATC	TCT	CAG	CAT	CAA	864
C	V	K	K	Q	C	P	E	N	S	G	C	F	R	H	L	D	E	306
TGC	GTG	AAG	AAG	CAA	TGT	CCC	GAG	AAT	TCA	GGT	TGC	TTC	CGC	CAC	TTA	GAC	GAA	918
R	E	E	C	K	C	L	L	N	Y	K	Q	E	G	D	K	C	V	324
AGG	GAG	GAA	TGT	AAA	TGC	CTG	CTG	AAT	TAT	AAA	CAG	GAA	GGA	GAC	AAG	TGC	GTA	972
E	N	P	N	P	T	C	N	E	N	N	G	G	C	D	A	D	A	342
GAG	AAT	CCT	AAC	CCA	ACC	TGT	AAC	GAA	AAT	AAC	GGT	GGC	TGC	GAT	GCT	GAC	GCT	1026
K	C	T	E	E	D	S	G	S	N	G	K	K	I	T	C	E	C	360
AAG	TGT	ACC	GAG	GAG	GAC	AGC	GGT	TCC	AAT	GGC	AAG	AAA	ATA	ACT	TGC	GAA	TGC	1080
T	K	P	D	S	Y	P	L	F	D	G	I	F	C	S	H	D	E	378
ACG	AAG	CCC	GAT	AGT	TAC	CCT	CTC	TTC	GAC	GGT	ATC	TTC	TGC	TCC	CAT	GAT	GAG	1134
L	*	E	L	T														383
CTT	TAA	GAG	CTC	ACC														1149

Fig. 9

Fig. 10

DNA AND AMINO ACID SEQUENCE OF BVp42-M

attggatccactaaa

13 atgtggtccttggaagtgtcttttattctgggctgtccttggtgacc
M W S W K C L L F W A V L V T
58 gccactctttgcacagcagcgatctctgttactatggacaacatc
A T L C T A A I S V T M D N I
103 ctcaagtggcttcgagaacgagtagcgcgtaatctacctaagccc
L S G F E N E Y D V I Y L K P
148 cttgccggtgtctaccgttcattgaagaaacagatagaaaagaat
L A G V Y R S L K K Q I E K N
193 attttcacgttcaacctcaacctaaatgacatcctcaactcgcgc
I F T F N L N L N D I L N S R
238 ctcaagaagcgaaaatacttcctcgacgtgttggaatccgacctt
L K K R K Y F L D V L E S D L
283 atgcaattttaagcacattagctctaacgagtacatcatagaggac
M Q F K H I S S N E Y I I E D
328 agcttcaagctcttgaattcagaacagaagaacaccctcctaag
S F K L L N S E Q K N T L L K
373 tcctacaaatacattaaggagtctgttgagaacgacatcaagttc
S Y K Y I K E S V E N D I K F
418 gcccaggaaggaattagctactatgagaaagtcctggctaaatac
A Q E G I S Y Y E K V L A K Y
463 aaggacgacttggaagcattaagaaggtaatcaaagaagagaag
K D D L E S I K K V I K E E K
508 gaaaagtttccgagctctccaccacaaactccccatcgccctgca
E K F P S S P P T T P P S P A
553 aagaccgacgagcagaaaaaagaaagtaagttccttccattcctc
K T D E Q K K E S K F L P F L
598 accaacatcgaaactctatataacaacctggtgaacaagattgat
T N I E T L Y N N L V N K I D
643 gactacttaatcaacttgaaggcgaaaattaatgactgtaacgtc
D Y L I N L K A K I N D C N V
688 gaaaaggatgaagcccacgttaagatcaccaagctttccgatctc
E K D E A H V K I T K L S D L
733 aaagccatcgacgataagattgacctgtttaagaaccacaacgat
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778 ttcgacgcaatcaaaaagttgatcaacgacgataactaagaagac
F D A I K K L I N D D T K K D
823 atgcttggaactgctgtcgacaggcttggtccaaaacttcccg
M L G K L L S T G L V Q N F P
868 aacaccattataagcaagctgatcgaaggaaagtttcaggatatg

1009514-0310

N T I I S K L I E G K F Q D M
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 L N I S Q H Q C V K K Q C P E
 958 aattcaggttgcttccgccacttagacgaaagggaggaatgtaaa
 N S G C F R H L D E R E E C K
 1003 tgcctgctgaattataaacaggaaggagacaagtgcgtagagaat
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 P N P T C N E N N G G C D A D
 1093 gctaagtgtaccgaggaggacagcggttccaatggcaagaaaata
 A K C T E E D S G S N G K K I
 1138 acttgcaatgcacgaagcccgatagttaccctctcttcgacggt
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 1183 atcttctgctcc
 I F C S

ccacctcatcatcatcatcatcattaataagggtaccta
 P P H H H H H H * *

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